

Amendments to the Specification

Please replace the paragraph at page 10, lines 1-12 with the following paragraph:

Peptides preferably have an amino acid sequence with at least 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, preferably 80-95% or more identity with the amino acid sequence of the PS peptide. The compound is optionally pharmaceutical grade purity (eg. for amino acids, this optionally means in excess of 99% purity, having a uniform crystalline structure, and white in color). Sequence identity is most preferably assessed by the BLAST version 2.1 program advanced search (parameters as above; Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403_410). BLAST is a series of programs that are available online at <http://www.ncbi.nlm.nih.gov/BLAST> from the National Center for Biotechnology Information (NCBI) of the U.S. National Institutes of Health. The advanced blast search (<http://www.ncbi.nlm.nih.gov/blast/blast.cgi?Jform=1>) is set to default parameters. (i.e. Matrix BLOSUM62; Gap existence cost 11; Per residue gap cost 1; Lambda ratio 0.85 default).